FIGURE 6A

Numbering is according to Kimura et al.

1. 'A' Allele, CYP2D6*3, A2637 deletion, Frameshift resulting in zero enzyme activity

2637

5'- G C T A A C T G A G C A C A G G A T G A C C -3' NH2	CYPwt(+)A2624,22mer,54%GC, Tm=63-64C
5'- G C T A A C T G A G C A C A G G A T G A C C (A)30-3' NH2	CYPwt(+)A2624(A)30-3'NH2
5'- C T A A C T G A G C A C A G G A T G A C C (A)30-3' NH2	CYPwt(+)A2625(A)30-3'NH2
5'- C T A A C T G A G C A C A G G A T G A C (A)30-3' NH2	CYPwt(+)A2625b(A)30-3'NH2
5'- C T A A C T G A G C A C A G G A T G A (A)30-3' NH2	CYPwt(+)A2625c(A)30-3'NH2
5'- G C T A A C T G A G C A C - G G A T G A C C -3' NH2	CYPmut(+)A2624,21mer,57%GC, Tm=61-63C
5'- G C T A A C T G A G C A C - G G A T G A C C (A)30-3' NH2	CYPmut(+)A2624(A)30-3'NH2
5'- C T A A C T G A G C A C - G G A T G A C C (A)30-3' NH2	CYPmut(+)A2625(A)30-3'NH2
5'- C T A A C T G A G C A C - G G A T G A C (A)30-3' NH2	CYPmut(+)A2625b(A)30-3'NH2
5'- C T A A C T G A G C A C - G G A T G A (A)30-3' NH2	CYPmut(+)A2625c(A)30-3'NH2
5'- g c t a a c t g a g c a c a g g a t g (A)30-3' NH2	CYPwt(+)A2624b(A)30-3'NH2
NH2 3'-(A)30 g a t t g a c t c g t g t c c t a c t g -5'	CYPwt(-)A2625(A)30-3'NH2
x= 2-Amino-dA 5'- c t g x g c a c x g g a t g x c (A)30-3' NH2	CYPwt(+)2629a(A)30-3'NH2
x= C-5 propynyl-C 5'- x t g a g x a c a g g a t g a x (A)30-3' NH2	CYPwt(+)2629b(A)30-3'NH2
-2612 x= C-5 propynyl-C 5'- x t g a g c a x a g g a t g a x (A)30-3' NH2	CYPwt(+)2629c(A)30-3'NH2
5'- G C T G G A T G A G C T G C T A A C T G A G C A C A G G A T G A C C T G G G A C C C A G C C C A G C C -3'	Wild Type (+)
5'- G C T G G A T G A G C T G C T A A C T G A G C A C - G G A T G A C C T G G G A C C C A G C C C A G C C -3'	Mut (+)

FIGURE 6B

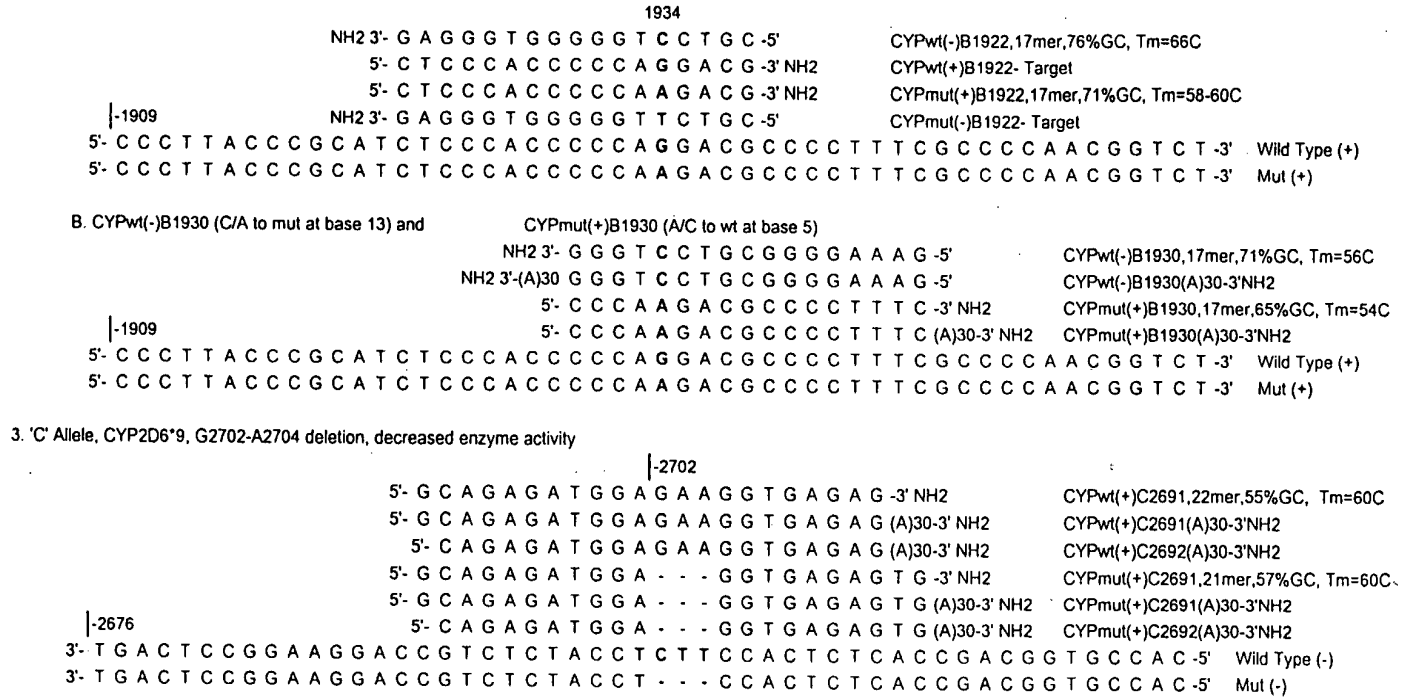

FIGURE 6C

4. 'E' Allele, CYP2D6*7, A3023C, H324P amino acid change results in zero enzyme activity

A. wt Probe - CYPwt(-)E3009 (T/C to mut at base 5) & CYPmut(+)E3009 (C/A to wt at base 15)

```
                                        3023
                NH2 3'- C G A G T A C T A G G A T G T A G G C -5'        CYPwt(-)E3009,19mer,53%GC,Pred Tm=57
          NH2 3'-(A)30 C G A G T A C T A G G A T G T A G G C -5'        CYPwt(-)E3009(A)30-3'NH2
                    5'- G C T C A T G A T C C T A C C T C C G -3' NH2   CYPmut(+)E3009,19mer,58%GC,Pred Tm=59C
 |-2998              5'- G C T C A T G A T C C T A C C T C C G (A)30-3' NH2   CYPmut(+)E3009(A)30-3'NH2
5'- T G G G G C C T C C T G C T C A T G A T C C T A C A T C C G G A T G T G C A G C|G T G A G C C C A T C -3'   Wild Type (+)
5'- T G G G G C C T C C T G C T C A T G A T C C T A C C T C C G G A T G T G C A G C|G T G A G C C C A T C -3'   Mut (+)
                                                                  |-3038-Intron Start
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B. CYPwt(-)E3018 (T/C to mut at base 14) and CYPmut(+)E3018 (C/T to wt at base 6)

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                                NH2 3'- G G A T G T A G G C C T A C A C G T C -5'   CYPwt(-)E3018,19mer,58%GC, Tm=60
                                  5'- C C T A C A T C C G G A T G T G C A G -3'     CYPwt(+)E3018- Target
                                  5'- C C T A C C T C C G G A T G T G C A G -3' NH2 CYPmut(+)E3018,19mer, 63%GC, Tm=62C
 |-2998                           3'- G G A T G G A G G C C T A C A C G T C -5'     CYPmut(-)E3018- Target
5'- T G G G G C C T C C T G C T C A T G A T C C T A C A T C C G G A T G T G C A G C|G T G A G C C C A T C -3'   Wild Type (+)
5'- T G G G G C C T C C T G C T C A T G A T C C T A C C T C C G G A T G T G C A G C|G T G A G C C C A T C -3'   Mut (+)
                                                                  |-3038-Intron Start
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5. 'G' Allele, CYP2D6*8, G1846T, Stop codon, zero enzyme activity

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                                        1846
                    5'- C A C T C C G G T G G G T G A T G G (A)30-3' NH2   CYPwt(+)G1840(A)30-3'NH2,18mer,67%GC, Tm=60
          NH2 3'-(A)30 G T G A G G C C A C C C A C T A C C -5'             CYPwt(-)G1840(A)30-3'NH2
                    5'- C A C T C C T G T G G G T G A T G G (A)30-3' NH2   CYPmut(+)G1840(A)30-3'NH2,18mer,61%GC, Tm=57
5'- G T G C C G C C T T C G C C A C T C C|G G T G G G T G A T G G G C A G A A G G G C A C A A A G C G G G -3'
5'- G T G C C G C C T T C G C C A C T C C|T G T G G G T G A T G G G C A G A A G G G C A C A A A G C G G G -3'
                          Exon 3 end-|-1846
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Replacement Sheet

FIGURE 6D

6. 'T' Allele, CYP2D6*6, T1795 deletion, Frameshift resulting in zero enzyme activity

	5'- G C T G G A G C A G T G G G T G A C -3' NH2	CYPwt(+)T1785,18mer,67%GC, Tm=59-61C
	5'- G C T G G A G C A G T G G G T G A C (A)30-3' NH2	CYPwt(+)T1785(A)30-3'NH2
	5'- C T G G A G C A G T G G G T G A C (A)30-3' NH2	CYPwt(+)T1786(A)30-3'NH2
	5'- G C T G G A G C A G - G G G T G A C -3' NH2	CYPmut(+)T1785,17mer,71%GC, Tm=58-60C
	5'- G C T G G A G C A G - G G G T G A C (A)30-3' NH2	CYPmut(+)T1785(A)30-3'NH2
|-1773	5'- C T G G A G C A G - G G G T G A C (A)30-3' NH2	CYPmut(+)T1786(A)30-3'NH2
5'- G G G C A A G A A G T C G C T G G A G C A G T G G G T G A C C G A G G A G G C C G C C T G C C T -3'		Wild Type (+)
5'- G G G C A A G A A G T C G C T G G A G C A G - G G G T G A C C G A G G A G G C C G C C T G C C T -3'		Mut (+)

7. 2D6/2D7/2D8 Controls - The 2D6/7/8 probes were designed in the 1600 region of the 2D6 gene. The purpose of the designs was to find region somewhere between the PCR primers were it would be easy to discriminate between 2D6 and its two pseudogenes, 2D7 and 2D8. The purpose of the designs is to demonstrate that the PCR amplicon is from the 2D6 gene, not one of the pseudogenes.

	5'- G A C C A G G G G G A G C - A T A G G (A)30-3' NH2	CYP2D6wt(+)1607(A)30-3'NH2
	5'- G A C C T T G T G G A G C G C C A G (A)30-3' NH2	CYP2D7wt(+)1607(A)30-3'NH2
	5'- G A C C A G G A A A A G C - A C A G G (A)30-3' NH2	CYP2D8wt(+)1607(A)30-3'NH2
1603- |	5'- G A C C A G G A A A A G C - A C A G G G (A)30-3' NH2	CYP2D8wt(+)1607b(A)30-3'NH2
5' G G G A G A C C A G G G G G A G C - A T A G G G T T G G A G T G G G T G G T -3'		2D6 (+)
5' G G G A G A C C T T G T G G A G C G C C A G G G T T G G A G T G G G T G G C -3'		2D7 (+)
5' G G G A G A C C A G G A A A A G C - A C A G G G T T G G A G T G G G C G G C -3'		2D8 (+)

8. Pos/Neg Control probes- These probes were designed as true positive and negative control probes. They consist of the same semi-random sequence, with the positive control probe having a 5' Biotin.

5' Biotin- A T C A T T C C A A T C A T C C A T A T C A T C (A)25-3' NH2	CYP(+)ran(A)25-5'Biotin,3'NH2
5'- A T C A T T C C A A T C A T C C A T A T C A T C (A)25-3' NH2	CYP(+)ran(A)25-3'NH2